

Response Under 37 CFR 1.116
Expedited Procedure
Examining Group 1600
Application No. 09/788,268
Paper Dated: December 23, 2004
In Reply to USPTO Correspondence of September 23, 2004
Attorney Docket No. 2087-010262

REMARKS

The Office Action of September 23, 2004 has been reviewed and the Examiner's comments carefully considered. The present Amendment cancels claims 81-91 in accordance and adds new claims 92-102. Claims 92-102 remain in this application. Applicant reserves the right to file at a later time a divisional application directed to the subject matter of non-elected Claim 80.

Applicant respectfully submits that the new claims do not contain new matter. The term "having suspected identity" has been removed from the new claims and replaced with the term "having homology", which term appears in the application as published [0132] , in [84] as originally filed, and in original claim 1.

The steps of calculating the masses of two or more polypeptides encoded in two or more reading frames of a defined DNA sequence to obtain a set of predicted mass values, and comparison of the predicted values with observed values, are recited multiple times in the application as originally filed:

(1) In the Abstract, it is stated: "A nucleic acid fragmentis expressed in one or more reading frames to produce one or more....polypeptides. The polypeptides are examined with respect to one or more physical parameters such as mass.... The observed parameter values are used to search a data set of *predicted* parameter values generated by hypothetical translation.....";

(2) In Example 1, pairs of polypeptides translated from the same polynucleotide are considered, and it is stated "The *predicted* amino acid sequence and molecular mass of eachtranslation product....is calculated, and the masses of the....possible polypeptides are tabulated..." ([0035] as published, [29] as filed), followed by "Comparison of the experimental results with the values in the table [i.e., with the pairs of calculated mass values] reveals a

Response Under 37 CFR 1.116
Expedited Procedure
Examining Group 1600
Application No. 09/788,268
Paper Dated: December 23, 2004
In Reply to USPTO Correspondence of September 23, 2004
Attorney Docket No. 2087-010262

match...." ([0037] as published,[31] as filed). Furthermore in the table itself, the column that shows the calculated mass values is headed "Predicted Peptide Mass".

(3) In Example 3, pairs of polypeptides are also translated from polynucleotide fragments, and it is stated that "the amino acid sequences of the two expected hybrid translation products....are calculated", after which "the mass of each peptide is calculated, andtabulated....". "Comparison of the experimental results (i.e., peptides of 4255 and 2635 Da) with the values *predicted* in the table indicates....."(both quotes taken from [46] as published, [39] as filed). Furthermore in the table in Example 3 itself, the column that shows the calculated mass values is headed "Predicted Peptide Mass".

(4) In Example 7 a predicted pair of masses is calculated for the peptides encoded in two reading frames of a polynucleotide, and pairs of masses are also calculated for the pairs of peptides encoded in all possible single nucleotide substitution variants of the polynucleotide. It is stated that the calculated (i.e., predicted) masses have "utility in the practice of the instant invention when searched.....using experimentally determined peptide mass data" ([0076] as published, [49] as filed). Further, it is stated that the process can be extended to more than two reading frames: "Indeed, when up to six reading frames are considered, there is little or no ambiguity for the great majority of substitutions, even for sequences as long as several hundred nucleotides" ([0075] as published, [48] as filed).

Response Under 37 CFR 1.116

Expedited Procedure

Examining Group 1600

Application No. 09/788,268

Paper Dated: December 23, 2004

In Reply to USPTO Correspondence of September 23, 2004

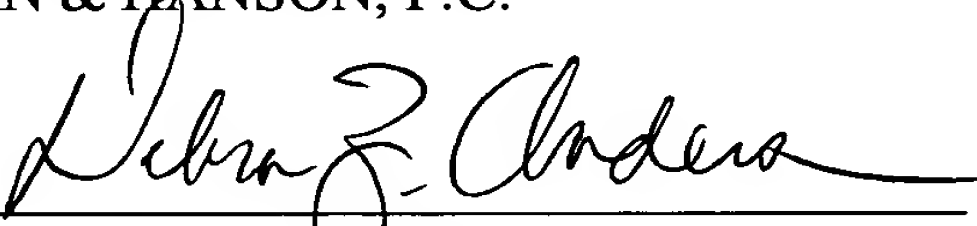
Attorney Docket No. 2087-010262

Based on these and other recitations in the original application, Applicant respectfully submits that the step of predicting the masses of polypeptides in two or more reading frames is described in the specification in a way that would be clear to one skilled in the relevant art. Inclusion of this step in the claims thus does not constitute the addition of new matter.

Applicant respectfully submits that all outstanding issues have been addressed, and claims 92-102 are in condition for allowance. Such action is respectfully requested at an early date.

Respectfully submitted,

WEBB ZIESENHEIM LOGSDON
ORKIN & HANSON, P.C.

By 

Debra Z. Anderson
Registration No. 44,506
Attorney for Applicant
700 Koppers Building
436 Seventh Avenue
Pittsburgh, PA 15219-1818
Telephone: (412) 471-8815
Facsimile: (412) 471-4094
E-mail: webblaw@webblaw.com